Signal peptide

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A **signal peptide** is a short (3-60 amino acids long) peptide chain that directs the post-translational transport of a protein. Signal peptides may also be called **targeting signals**, **signal sequences**, **transit peptides**, or **localization signals**.

The amino acid sequences of signal peptides direct proteins (which are synthesized in the cytosol) to certain organelles such as the nucleus, mitochondrial matrix, endoplasmic reticulum, chloroplast, and peroxisome. Some signal peptides are cleaved from the protein by *signal peptidase* after the proteins are transported.

Contents

ER signal peptide

An endoplasmic reticulum signal peptide is the best characterised signal peptide. It exists at the amino terminal of a protein. The protein is guided to the ER by a signal-recognition particle, which moves between the ER and the cytoplasm. It binds to the signal peptide. The SRP binds to the signal peptide as soon as it is synthesised and extruded from the ribosome. This causes a pause in protein synthesis, most probably allowing the ribosome-SRP complex time to bind to the SRP receptor on the target ER membrane. The SRP protein is thought to be a regulatory GTP protein. Conformational changes may therefore lead to the SRP release. The protein may then be threaded through the ER membrane by a translocator pore.

Nuclear signal peptides

A *nuclear localization signal* (NLS) is a signal peptide directing to the nucleus and is often a unit consisting of plus-charged amino acids. The NLS normally is located inside the peptide chain. Almost all proteins that are transported to the endoplasmic reticulum have a sequence consisting of 5-10 hydrophobic amino acids on the N-terminus. Most of these proteins are transported from the endoplasmic reticulum to the Golgi apparatus. If these proteins have a particular 4-amino-acids sequence on the C-terminus, these proteins stay in the endoplasmic reticulum.

The nucleolus within the nucleus can be targeted with a sequence called a *nucleolar localization signal* (abbreviated NoLS or NOS).

The signal peptide that directs to the mitochondrial matrix has a sequence consisting of an alternating

pattern with a few hydrophobic amino acids and a few plus-charged amino acids form. It is usually called the *mitochondrial targeting signal* (MTS).

There are two types of signal peptides directing to peroxisome, which are called *peroxisomal targeting signals* (PTS). One is PTS1, which is made of three amino acids on the C-terminus. The other is PTS2, which is made of a 9-amino-acid sequence often present on the N-terminus of the protein.

Types

Following is a list of types of signal peptides:

- N-terminus signal peptides often target the mitochondrial matrix, endoplasmic reticulum and peroxisome.
- C-terminus signal peptides often target the peroxisome.

Typical signal peptides

Transport to the nucleus (NLS)	-Pro-Pro-Lys-Lys-Lys-Arg-Lys-Val-
Transport to the endoplasmic reticulum	H_2N-Met-Met-Ser-Phe-Val-Ser-Leu-Leu-Leu-Val-Gly-Ile-Leu-Phe-Trp-Ala-Thr-Glu-Ala-Glu-Gln-Leu-Thr-Lys-Cys-Glu-Val-Phe-Gln-
Retention to the endoplasmic reticulum	-Lys-Asp-Glu-Leu-COOH
Transport to the mitochondrial matrix	H_2N-Met-Leu-Ser-Leu-Arg-Gln-Ser-Ile-Arg-Phe-Phe-Lys-Pro-Ala-Thr-Arg-Thr-Leu-Cys-Ser-Ser-Arg-Tyr-Leu-Leu-
Transport to the peroxisome (PTS1)	-Ser-Lys-Leu-COOH
Transport to the peroxisome (PTS2)	H_2N-----Arg-Leu-X_5-His-Leu-

H_2N is the N-terminus of a protein. COOH is the C-Terminus of a protein.

See also

- Protein targeting

External links

- MeSH *Signal+Peptide (http://www.nlm.nih.gov/cgi/mesh/2007/MB_cgi?mode=&term=Signal+Peptide)*

Retrieved from "http://en.wikipedia.org/wiki/Signal_peptide"

Categories: Cell signaling | Gene expression

signal sequence

Definition:

The N-terminal sequence of a secreted protein, which is required for transport through the cell membi

A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

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Note: Performing your original search, ***signal sequence cleavage***, in PubMed will retrieve ***1304*** citations.

1: Nucleic Acids Res. 1986 Jun 11;14(11):4683-90.

A new method for predicting signal sequence cleavage sites.

von Heijne G.

A new method for identifying secretory signal sequences and for predicting the site of cleavage between a signal sequence and the mature exported protein is described. The predictive accuracy is estimated to be around 75-80% for both prokaryotic and eukaryotic proteins.

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